

AMENDMENTS TO THE CLAIMS

1. (Currently amended) A method of identifying genetic mutations that are associated with ataxic neurological disease in a ~~mammalian~~ human subject, said method comprising:

(a) determining a first nucleic acid sequence of a human protein kinase C gamma gene from a first human subject exhibiting ataxia;

(b) identifying a difference between [[a]] the first nucleic acid sequence of a ~~protein kinase C gamma gene~~ from [[a]] the first ~~mammalian~~ human subject exhibiting ataxia and SEQ ID NO:3 a second nucleic acid sequence of a ~~protein kinase C gamma gene~~ from a second ~~mammalian~~ subject which is not exhibiting ataxia, wherein the first and second ~~mammalian~~ subjects are members of the same species, and wherein the difference between the nucleic acid sequences represents a genetic mutation in the first nucleic acid sequence that is associated with ataxic neurological disease; and

(c) confirming that the difference identified between the first nucleic acid sequence and SEQ ID NO:3 is a genetic mutation associated with ataxia by co-segregation analysis comprising determining that the identified nucleic acid sequence difference is also present in a plurality of human subjects exhibiting ataxia and is absent in a plurality of human subjects not exhibiting ataxia.

2. (Currently amended) The method of Claim 1 wherein the first nucleic acid sequence ~~[[of]]~~ from said first human subject ~~and said second subject~~ is determined by amplification of portions of the human protein kinase C gamma ~~[[genes]]~~ gene from genomic DNA isolated from said ~~subjects~~ human subject to produce an amplified DNA and sequencing said amplified DNA.

3. (Canceled)

4. (Currently amended) The method of [[Claim 3]] Claim 1 wherein said cosegregation ~~is detected by analysis~~ comprises a method selected from the group consisting of direct sequencing, sequencing PCR-amplified DNA, single stranded conformation analysis, allele-specific PCR and restriction fragment length polymorphism.

5. (Currently amended) The method of Claim 4 wherein said cosegregation ~~is detected by analysis~~ comprises sequencing PCR-amplified DNA.

6. (Currently amended) The method of Claim 4 wherein said cosegregation ~~is detected by analysis~~ comprises restriction fragment length polymorphism ~~wherein the presence of an aberrant restriction enzyme site is indicative of the presence of said genetic mutation and cosegregation is determined by the presence of said genetic mutation in a first population of mammalian subjects that exhibit ataxia and not present in a second population of subjects that do not exhibit ataxia.~~

7-42. (Canceled)

43. (New) The method of Claim 2, wherein the portions of nucleic acid sequence that are amplified comprises at least one of exon 1 (nucleotides 440 to 609 of SEQ ID NO:3); exon 2 (nucleotides 1108 to 1139 of SEQ ID NO:3); exon 3 (nucleotides 2106 to 2188 of SEQ ID NO:3); exon 4 (nucleotides 7583 to 7694 of SEQ ID NO:3); exon 5 (nucleotides 7831 to 7962 of SEQ ID NO:3); exon 6 (nucleotides 9619 to 9775 of SEQ ID NO:3); exon 7 (nucleotides 10454 to 10588 of SEQ ID NO:3); exon 8 (nucleotides 10933 to 11020 of SEQ ID NO:3); exon 9 (nucleotides 11307 to 11336 of SEQ ID NO:3); exon 10 (nucleotides 15904 to 16056 of SEQ ID NO:3); exon 11 (nucleotides 16385 to 16573 of SEQ ID NO:3); exon 12 (nucleotides 18178 to 18269 of SEQ ID NO:3); exon 13 (nucleotides 18364 to 18426 of

SEQ ID NO:3); exon 14 (nucleotides 18556 to 18694 of SEQ ID NO:3); exon 15 (nucleotides 21018 to 21098 of SEQ ID NO:3); exon 16 (nucleotides 22580 to 22687 of SEQ ID NO:3); exon 17 (nucleotides 24262 to 24402 of SEQ ID NO:3); or exon 18 (nucleotides 24652 to 24840 of SEQ ID NO:3).

44. (New) The method of Claim 43, wherein the portion of SEQ ID NO:3 that is amplified comprises exon 4 (nucleotides 7583 to 7694 of SEQ ID NO:3).

45. (New) The method of Claim 1, wherein the mutation associated with ataxia neurological disease is selected from the group consisting of a missense mutation, a deletion mutation, an insertion mutation, a splicing site mutation, and a mutation that results in loss of expression of the protein kinase C gamma gene encoded by SEQ ID NO:3.

46. (New) The method of Claim 45, wherein the mutation is a missense mutation.